

SEQUENCE LISTING

<110> Mr. Hitoshi ENDO

<120> ORGANIC ANION TRANSPORTER AND GENE CODING FOR THE SAME

<160> 2

<210> 1

<211> 2294

<212> DNA

<213> Rat

<223> Number of Chain : Doubled-Stranded

Topology : Linear

Kind : cDNA to mRNA

GCTCCAGCAG ACCCTGAAAG CTGAGCTGTC CAGACCCCCG AAGTGAAGAA AAGAGGCGAG	60
GGCAAGGGAG GGCCAGAACC GAGGGAGAGA GAAAGGAGGG GCAGCCCACC AGCCCGCTGT	120
CCTGCCACAG AACCGGCTCA GCTCCAGCTC CAGGAGTCAC TCAGCTGCAG AGGCAGTGGC	180
AGCCCCACTC CTCAGGCAAA GGGCAGCAGA CAGACAGACA GAGGTCCTAG GACTGGAGGT	240
CCTCAGTCAT TGACCACTCA GCCTGGCCCA GCCCC	275
ATG GCC TTC AAT GAC CTC CTG AAA CAG GTG GGG GGC GTC GGA CGC	320
Met Ala Phe Asn Asp Leu Leu Lys Gln Val Gly Gly Val Gly Arg	
1 5 10 15	
TTC CAG TTG ATC CAG GTC ACC ATG GTG GTT GCT CCC CTA CTG CTG	365
Phe Gln Leu Ile Gln Val Thr Met Val Val Ala Pro Leu Leu Leu	
20 25 30	
ATG GCT TCC CAC AAC ACC TTG CAG AAC TTC ACT GCC GCT ATC CCC	410
Met Ala Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro	
35 40 45	

CCT CAT CAC TGC CGC CCA CCT GCC AAT GCC AAT CTC AGC AAA GAT	455
Pro His His Cys Arg Pro Pro Ala Asn Ala Asn Leu Ser Lys Asp	
50 55 60	
GGA GGT CTG GAG GCC TGG CTG CCC CTG GAC AAG CAA GGA CAA CCC	500
Gly Gly Leu Glu Ala Trp Leu Pro Leu Asp Lys Gln Gly Gln Pro	
65 70 75	
GAA TCG TGC CTC CGC TTT ACT TCC CCC CAG TGG GGA CCA CCC TTT	545
Glu Ser Cys Leu Arg Phe Thr Ser Pro Gln Trp Gly Pro Pro Phe	
80 85 90	
TAC AAT GGC ACA GAA GCC AAT GGC ACC AGA GTC ACA GAG CCC TGC	590
Tyr Asn Gly Thr Glu Ala Asn Gly Thr Arg Val Thr Glu Pro Cys	
95 100 105	
ATT GAT GGC TGG GTC TAT GAC AAC AGC ACC TTC CCT TCA ACC ATC	635
Ile Asp Gly Trp Val Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile	
110 115 120	
GTG ACT GAG TGG AAC CTT GTG TGC TCT CAT CGG GCT TTC CGC CAG	680
Val Thr Glu Trp Asn Leu Val Cys Ser His Arg Ala Phe Arg Gln	
125 130 135	
CTG GCC CAG TCC CTG TAC ATG GTG GGA GTG CTG CTG GGA GCC ATG	725
Leu Ala Gln Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met	
140 145 150	
GTG TTT GGC TAC CTG GCG GAC AGG CTG GGC CGC CGG AAG GTG CTG	770
Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly Arg Arg Lys Val Leu	
155 160 165	
ATC TTG AAC TAC CTG CAG ACA GCT GTG TCG GGA ACC TGT GCA GCC	815
Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly Thr Cys Ala Ala	
170 175 180	
TAT GCA CCC AAC TAT ACT GTC TAC TGC GTT TTC CGG CTC CTC TCG	860

Tyr Ala Pro Asn Tyr Thr Val Tyr Cys Val Phe Arg Leu Leu Ser	
185	190 195
GGC ATG TCT TTG GCT AGC ATT GCA ATC AAC TGC ATG ACA CTA AAT	905
Gly Met Ser Leu Ala Ser Ile Ala Ile Asn Cys Met Thr Leu Asn	
200	205 210
GTG GAA TGG ATG CCT ATC CAC ACC CGT GCC TAT GTG GGC ACC TTG	950
Val Glu Trp Met Pro Ile His Thr Arg Ala Tyr Val Gly Thr Leu	
215	220 225
ATT GGC TAT GTC TAC AGC CTG GGC CAG TTC CTC CTG GCT GGC ATC	995
Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Ile	
230	235 240
GCC TAT GCT GTG CCC CAC TGG CGC CAC CTG CAG CTT GTG GTC TCT	1040
Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Val Val Ser	
245	250 255
GTG CCT TTT TTC ATT GCC TTC ATC TAC TCT TGG TTC TTC ATT GAG	1085
Val Pro Phe Phe Ile Ala Phe Ile Tyr Ser Trp Phe Phe Ile Glu	
260	265 270
TCA GCC CGC TGG TAC TCC TCC TCA GGA AGG CTG GAC CTC ACC CTC	1130
Ser Ala Arg Trp Tyr Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu	
275	280 285
CGA GCC CTG CAG AGA GTG GCC CGG ATC AAT GGG AAA CAA GAA GAA	1175
Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys Gln Glu Glu	
290	295 300
GGG GCT AAG CTA AGT ATA GAG GTG CTC CGG ACC AGC CTG CAG AAG	1220
Gly Ala Lys Leu Ser Ile Glu Val Leu Arg Thr Ser Leu Gln Lys	
305	310 315
GAA CTG ACT CTA AGC AAA GGC CAA GCC TCA GCC ATG GAG CTG CTG	1265
Glu Leu Thr Leu Ser Lys Gly Gln Ala Ser Ala Met Glu Leu Leu	

320	325	330	
CGC TGC CCC ACC CTT CGA CAC CTC TTC CTC TGT CTC TCC ATG CTG			1310
Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu			
335	340	345	
TGG TTT GCC ACT AGC TTT GCC TAC TAC GGG CTG GTC ATG GAC CTG			1355
Trp Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu			
350	355	360	
CAG GGC TTT GGG GTC AGC ATG TAC CTT ATC CAG GTG ATT TTC GGT			1400
Gln Gly Phe Gly Val Ser Met Tyr Leu Ile Gln Val Ile Phe Gly			
365	370	375	
GCC GTG GAC CTG CCT GCC AAG TTT GTA TGC TTC CTA GTC ATC AAC			1445
Ala Val Asp Leu Pro Ala Lys Phe Val Cys Phe Leu Val Ile Asn			
380	385	390	
TCC ATG GGG CGC CGG CCT GCA CAG ATG GCC TCC CTG CTG CTG GCA			1490
Ser Met Gly Arg Arg Pro Ala Gln Met Ala Ser Leu Leu Leu Ala			
395	400	405	
GGC ATC TGC ATC CTG GTG AAT GGC ATA ATA CCG AAG AGC CAT ACG			1535
Gly Ile Cys Ile Leu Val Asn Gly Ile Ile Pro Lys Ser His Thr			
410	415	420	
ATC ATT CGC ACC TCC CTG GCT GTG CTA GGG AAG GGC TGC CTG GCT			1580
Ile Ile Arg Thr Ser Leu Ala Val Leu Gly Lys Gly Cys Leu Ala			
425	430	435	
TCC TCT TTC AAC TGC ATC TTC CTG TAC ACC GGA GAG CTG TAC CCC			1625
Ser Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu Tyr Pro			
440	445	450	
ACA GTG ATT CGG CAG ACA GGC CTG GGC ATG GGC AGC ACC ATG GCC			1670
Thr Val Ile Arg Gln Thr Gly Leu Gly Met Gly Ser Thr Met Ala			
455	460	465	

CGG GTG GGC AGC ATT GTG AGC CCG CTG GTG AGC ATG ACT GCA GAG 1715
Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu

470 475 480

TTC TAC CCC TCC ATG CCT CTC TTC ATC TTC GGC GCT GTC CCT GTG 1760
Phe Tyr Pro Ser Met Pro Leu Phe Ile Phe Gly Ala Val Pro Val

485 490 495

GTC GCC AGT GCT GTC ACT GCC CTG CTG CCA GAG ACC TTG GGC CAG 1805
Val Ala Ser Ala Val Thr Ala Leu Leu Pro Glu Thr Leu Gly Gln

500 505 510

CCG CTG CCA GAT ACA GTG CAG GAC CTG AAG AGC AGG AGC AGA GGA 1850
Pro Leu Pro Asp Thr Val Gln Asp Leu Lys Ser Arg Ser Arg Gly

515 520 525

AAG CAG AAT CAA CAG CAG CAG GAA CAG CAG AAG CAG ATG ATG CCG 1895
Lys Gln Asn Gln Gln Gln Gln Glu Gln Gln Lys Gln Met Met Pro

530 535 540

CTC CAG GCC TCA ACA CAA GAG AAG AAT GGA CTT 1928
Leu Gln Ala Ser Thr Gln Glu Lys Asn Gly Leu

545 550 551

TGAGAACGGA AGGGCTTCAC ACAGCACTAA AGGGAGTGGG GTTCTACAGG TCCTGCCGTC 1988

TACATGAGGA GGGGGAGTGA GTAGAGGGAC TGGACCATCC AAATGTGGAG GCTGCCATTC 2048

AGAGAAATCC CTCCCCAAAG GTCATGTCAG TAGACCCACT AGGAACAAAA GCTCTGACTA 2108

TGTGCAGCTT CTTAAGCAGA ATGTTCTCGT CACCGGCCAT CTTCTGCTC ATGGTCACTC 2168

CGCCACCTCC AGGACCTTGC AAAGAATCTC AGACAATTAA ATGAATCTCT TCTAAAAAAA 2228

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2288

AAAAAA 2294

<210> 2

<211> 2171

<212> DNA

<213> Human

<223> Number of Chain : Doubled-Stranded

Topology : Linear

Kind : cDNA to mRNA

GAAAGCTGAG CTGCCCTGAC CCCCAAAGTG AGGAGAAGCT GCAAGGGAAA AGGGAGGGAC 60
AGATCAGGGA GACCGGGGAA GAAGGAGGAG CAGCCAAGGA GGCTGCTGTC CCCCCACAGA 120
GCAGCTCGGA CTCAGCTCCC GGAGCAACCC AGCTGCGGAG GCAACGGCAG TGCTGCTCCT 180
CCAGCGAAGG ACAGCAGGCA GGCAGACAGA CAGAGGTCCT GGGACTGGAA GGCCTCAGCC 240
CCCAGCCACT GGGCTGGGCC TGGCCCA 267
ATG GCC TTT AAT GAC CTC CTG CAG CAG GTG GGG GGT GTC GGC CGC 312
Met Ala Phe Asn Asp Leu Leu Gln Gln Val Gly Gly Val Gly Arg
1 5 10 15
TTC CAG CAG ATC CAG GTC ACC CTG GTG GTC CTC CCC CTG CTC CTG 357
Phe Gln Gln Ile Gln Val Thr Leu Val Val Leu Pro Leu Leu Leu
20 25 30
ATG GCT TCT CAC AAC ACC CTG CAG AAC TTC ACT GCT GCC ATC CCT 402
Met Ala Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro
35 40 45
ACC CAC CAC TGC CGC CCG CCT GCC GAT GCC AAC CTC AGC AAG AAC 447
Thr His His Cys Gly Pro Pro Ala Asp Ala Asn Leu Ser Lys Asn
50 55 60
GGG GGG CTG GAG GTC TGG CTG CCC CGG GAC AGG CAG GGG CAG CCT 492
Gly Gly Leu Glu Val Trp Leu Pro Arg Asp Arg Gln Gly Gln Pro
65 70 75
GAG TCC TGC CTC CGC TTC ACC TCC CCG CAG TGG GGA CTG CCC TTT 537
Glu Ser Cys Leu Arg Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe

	80	85	90	
CTC AAT GGC ACA GAA GCC AAT GGC ACA GGG GCC ACA GAG CCC TGC				582
Leu Asn Gly Thr Glu Ala Asn Gly Thr Gly Ala Thr Glu Pro Cys				
	95	100	105	
ACC GAT GGC TGG ATC TAT GAC AAC AGC ACC TTC CCA TCT ACC ATC				627
Thr Asp Gly Trp Ile Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile				
	110	115	120	
GTG ACT GAG TGG GAC CTT GTG TGC TCT CAC AGG GCC CTA CGC CAG				672
Val Thr Glu Trp Asp Leu Val Cys Ser His Arg Ala Leu Arg Gln				
	125	130	135	
CTG GCC CAG TCC TTG TAC ATG GTG GGG GTG CTG CTC GGA GCC ATG				717
Leu Ala Gln Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met				
	140	145	150	
GTG TTC GGC TAC CTT GCA GAC AGG CTA GGC CGC CGG AAG GTA CTC				762
Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly Arg Arg Lys Val Leu				
	155	160	165	
ATC TTG AAC TAC CTG CAG ACA GCT GTG TCA GGG ACC TGC GCA GCC				807
Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly Thr Cys Ala Arg				
	170	175	180	
TTC GCA CCC AAC TTC CCC ATC TAC TGC GCC TTC CGG CTC CTC TCG				852
Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg Leu Leu Ser				
	185	190	195	
GGC ATG GCT CTG GCT GGC ATC TCC CTC AAC TGC ATG ACA CTG AAT				897
Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr Leu Asn				
	200	205	210	
GTG GAG TGG ATG CCC ATT CAC ACA CGG GCC TGC GTG GGC ACC TTG				942
Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr Leu				
	215	220	225	

ATT GGC TAT GTC TAC AGC CTG GGC CAG TTC CTC CTG GCT GGT GTG	987
Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val	
230 235 240	
GCC TAC GCT GTG CCC CAC TGG CGC CAC CTG CAG CTA CTG GTC TCT	1032
Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser	
245 250 255	
GCG CCT TTT TTT GCC TTC TTC ATC TAC TCC TGG TTC TTC ATT GAG	1077
Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu	
260 265 270	
TCG GCC CGC TGG CAC TCC TCC TCC GGG AGG CTG GAC CTC ACC CTG	1122
Ser Ala Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu	
275 280 285	
AGG GCC CTG CAG AGA GTC GCC CGG ATC AAT GGG AAG CGG GAA GAA	1167
Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu	
290 295 300	
GGA GCC AAA TTG AGT ATG GAG GTA CTC CGG GCC AGT CTG CAG AAG	1212
Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu Gln Lys	
305 310 315	
GAG CTG ACC ATG GGC AAA GGC CAG GCA TCG GCC ATG GAG CTG CTG	1257
Glu Leu Thr Met Gly Lys Gly Gln Ala Ser Ala Met Glu Leu Leu	
320 325 330	
CGC TGC CCC ACC CTC CGC CAC CTC TTC CTC TGC CTC TCC ATG CTG	1302
Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu	
335 340 345	
TGG TTT GCC ACT AGC TTT GCA TAC TAT GGG CTG GTC ATG GAC CTG	1347
Trp Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu	
350 355 360	
CAG GGC TTT GGA GTC AGC ATC TAC CTA ATC CAG GTG ATC TTT GGT	1392

Gln Gly Phe Gly Val Ser Ile Tyr Leu Ile Gln Val Ile Phe Gly	
365 370 375	
GCT GTG GAC CTG CCT GCC AAG CTT GTG GGC TTC CTT GTC ATC AAC	1437
Ala Val Asp Leu Pro Ala Lys Leu Val Gly Phe Leu Val Ile Asn	
380 385 390	
TCC CTG GGT CGC CGG CCT GCC CAG ATG GCT GCA CTG CTG CTG GCA	1482
Ser Leu Gly Arg Arg Pro Ala Gln Met Ala Ala Leu Leu Leu Ala	
395 400 405	
GGC ATC TGC ATC CTG CTC AAT GGG GTG ATA CCC CAG GAC CAG TCC	1527
Gly Ile Cys Ile Leu Leu Asn Gly Val Ile Pro Gln Asp Gln Ser	
410 415 420	
ATT GTC CGA ACC TCT CTT GCT GTG CTG GGG AAG GGT TGT CTG GCT	1572
Ile Val Arg Thr Ser Leu Ala Val Leu Gly Lys Gly Cys Leu Ala	
425 430 435	
GCC TCC TTC AAC TGC ATC TTC CTG TAT ACT GGG GAA CTG TAT CCC	1617
Ala Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu Tyr Pro	
440 445 450	
ACA ATG ATC CGG CAG ACA GGC ATG GGA ATG GGC AGC ACC ATG GCC	1662
Thr Met Ile Arg Gln Thr Gly Met Gly Met Gly Ser Thr Met Ala	
455 460 465	
CGA GTG GGC AGC ATC GTG AGC CCA CTG GTG AGC ATG ACT GCC GAG	1707
Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu	
470 475 480	
CTC TAC CCC TCC ATG CCT CTC TTC ATC TAC GGT GCT GTT CCT GTG	1752
Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr Gly Ala Val Pro Val	
485 490 495	
GCC GCC AGC GCT GTC ACT GTC CTC CTG CCA GAG ACC CTG GGC CAG	1797
Ala Ala Ser Ala Val Thr Val Leu Leu Pro Glu Thr Leu Gly Gln	

500	505	510	
CCA CTG CCA GAC ACG GTG CAG GAC CTG GAG AGC AGG TGG GCC CCC			1842
Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser Arg Trp Ala Pro			
515	520	525	
ACT CAG AAA GAA GCA GGG ATA TAT CCC AGG AAA GGG AAA CAG ACG			1887
Thr Gln Lys Glu Ala Gly Ile Tyr Pro Arg Lys Gly Lys Gln Thr			
530	535	540	
CGA CAG CAA CAA GAG CAC CAG AAG TAT ATG GTC CCA CTG CAG GCC			1932
Arg Gln Gln Gln Glu His Gln Lys Tyr Met Val Pro Leu Gln Ala			
545	550	555	
TCA GCA CAA GAG AAG AAT GGA CTC			1956
Ser Ala Gln Glu Lys Asn Gly Leu			
560	563		
TGAGGACTGA GAAGGGGCCT TACAGAACCC TAAAGGGAGG GAAGGTCCTA CAGGTCTCCG			2016
GCCACCCACA CAAGGAGGAG GAAGAGGAAA TGGTGACCCA AGTGTGGGGG TTGTGGTTCA			2076
GGAAAGCATC TTCCAGGGG TCCACCTCCC TTTATAAACC CCACCAGAAC CACATCATT			2136
AAAGGTTTGA CTGCGAAAAA AAAAAAAAAA AAAAA			2171